

	SEQUENCE LISTING
<110>	Bertin, John Manji, Gulam A.
<120>	NOVEL MOLECULES OF THE PYRIN DOMAIN PROTEIN FAMILY AND USES THEREOF
<130>	07334-341001
	US 10/027,629 2001-12-20
	US 09/964,955 2001-09-26
	US 09/653,901 2000-09-01
	US 09/506,067 2000-02-17
<160>	17
<170>	FastSEQ for Windows Version 4.0
<210><211><211><212><213>	3431
<220> <221> <222>	CDS (78)(3176)
	l ctcat ctccgccggc gagtagggcc aggtgttggg agctcccacg tgggacaagg tcttc ggcgcag atg ggt ttc aac ctg cag gct ctc ctg gag cag Met Gly Phe Asn Leu Gln Ala Leu Leu Glu Gln

< 400)> 1															
				cag a	atg q	ggt t	itc a	aac (etg (cag (gct (ctc d	ctg (tggga gag o Glu o 10	g	60 110
	-	-	_	-	-	_	_		_		_		-	acc Thr		158
														gac Asp		206
														gac Asp		254
														cac His		302

_	-	-			-	_	-	-	-	-	-	-	-	gct Ala 90	_	350
						_					,,,			cgg Arg		398
														aaa Lys		446
														acg Thr		494
														gtc Val		542
														ccc Pro 170		590
														cct Pro		638
														tgg Trp		686
	_									_				agc Ser	-	734
			_	-			_	•	-		-		_	gtc Val		782
	-			-	-	_	-	_						gcc Ala 250		830
														gga Gly		878
														aag Lys		926
														atg Met		974

Pro		gcc Ala			Leu					Pro					Asp	1022
300					305					310					315	
		atc Ile														1070
		gag Glu														1118
		gcc Ala 350														1166
		ctg Leu														1214
		ctg Leu														1262
		acg Thr														1310
		cag Gln														1358
		ctg Leu 430			_	_					_		-			1406
		ggg Gly														1454
		cgc Arg														1502
		ttc Phe														1550
		gaa Glu		-		-					-			_	_	1598
		ctg Leu 510														1646
caa	gca	ggc	tac	tac	tcc	ttt	ggc	ctc	gct	aac	gag	aag	aga	gcc	aag	1694

					•					4						
Gln	Ala 525	Gly	Tyr	Tyr	Ser	Phe 530	Gly	Leu	Ala	Asn	Glu 535	Lys	Arg	Ala	Lys	
						ggc Gly					_	-			_	1742
						ata Ile										1790
						ctc Leu										1838
	_		_			atg Met	_				_			_		1886
						gtg Val 610										1934
						tca Ser										1982
						gaa Glu										2030
						cct Pro										2078
						atg Met										2126
						atc Ile 690										2174
						gtg Val										2222
						gct Ala										2270
						gac Asp										2318
						gaa Glu										2366

		750					755				760				
					act Thr									2	414
					ctg Leu 785			-			-			2	462
		-			aag Lys	_	_			_	_		-	2	510
					ttg Leu									2	558
					gct Ala									2	606
	_	-	_	_	aag Lys							 -		2	654
					agg Arg 865									2	702
					ata Ile									2	750
					tca Ser									2	798
					gga Gly									2	846
					aga Arg									2	894
					gac Asp 945					-				2	942
					ggt Gly									2	990
_	_		_		ttg Leu		_		 					3	038

			Ile					Asp					Leu	ctg Leu		3086
		Glu					Gln					Thr		aaa Lys		3134
	Pro		gca Ala			Pro					Phe					3176
tgcc gcta ttac	ctgto agato cata	gac gtt tga	tcct ttag	ctcc ccat tctg	to co ga ti	ccgg tctg	cace:	t ac t gt	cccto ttta	cagg tacc	gata tgca	aatga acac	agt atc	tcat ctta	gtgaac tgctgg tctttg attcac	3236 3296 3356 3416 3431
<211 <212	0> 2 1> 10 2> P1 3> Ho	RT	sapi	ens												
Met)> 2 Gly	Phe	Asn		Gln	Ala	Leu	Leu		Gln	Leu	Ser	Gln	Asp	Glu	
l Leu	Ser	Lys		5 Lys	Tyr	Leu	Ile		10 Thr	Phe	Ser	Pro		15 His	Glu	
Leu	Gln	Lys 35	20 Ile	Pro	His	Lys	Glu 40	25 Val	Asp	Lys	Ala	Asp	30 Gly	Lys	Gln	
Leu	Val 50		Ile	Leu	Thr	Thr 55		Cys	Asp	Ser	Tyr 60		Val	Glu	Met	
Ala 65		Leu	Gln	Val	Phe 70		Lys	Met	His	Arg 75		Asp	Leu	Ser	Glu 80	
Arg	Ala	Lys	Asp	Glu 85	Val	Arg	Glu	Ala	Ala 90	Leu	Lys	Ser	Phe	Asn 95	Lys	
	_		100			_		105	-	•		_	110	Pro		
		115					120					125		Asp		
	130					135					140			Met		
Lys 145	Ser	Trp	Pro	Gly	Asp 150	Ser	Lys	Glu	Val	Gln 155	Val	Met	Ala	Glu	Arg 160	
Tyr	Lys	Met	Leu	Ile 165	Pro	Phe	Ser	Asn	Pro 170	Arg	Val	Leu	Pro	Gly 175	Pro	
Phe	Ser	Tyr	Thr 180	Val	Val	Leu	Tyr	Gly 185	Pro	Ala	Gly	Leu	Gly 190	Lys	Thr	
Thr	Leu	Ala 195	Gln	Lys	Leu	Met	Leu 200	Asp	Trp	Ala	Glu	Asp 205	Asn	Leu	Ile	
His	Lys 210	Phe	Lys	Tyr	Ala	Phe 215	Tyr	Leu	Ser	Cys	Arg 220		Leu	Ser	Arg	
Leu 225	Gly	Pro	Cys	Ser	Phe 230	Ala	Glu	Leu	Val	Phe 235	Arg	Asp	Trp	Pro	Glu 240	
Leu	Gln	Asp	Asp	Ile 245	Pro	His	Ile	Leu	Ala 250		Ala	Arg	Lys	Ile 255		

Phe	Val	Ile	Asp 260	Gly	Phe	Asp	Glu	Leu 265	Gly	Ala	Ala	Pro	Gly 270	Ala	Leu
Ile	Glu	Asp 275	Ile	Cys	Gly	Asp	Trp 280	Glu	Lys	Lys	Lys	Pro 285		Pro	Val
Leu	Leu 290	Gly	Ser	Leu	Leu	Asn 295	Arg	Val	Met	Leu	Pro 300	Lys	Ala	Ala	Leu
Leu 305	Val	Thr	Thr	Arg	Pro 310		Ala	Leu	Arg	Asp 315		Arg	Ile	Leu	Ala 320
Glu	Glu	Pro	Ile	Tyr 325	Ile	Arg	Val	Glu	Gly 330	Phe	Leu	Glu	Glu	Asp 335	
Arg	Ala	Tyr	Phe 340	Leu	Arg	His	Phe	Gly 345	Asp	Glu	Asp	Gln	Ala 350	Met	Arg
Ala	Phe	Glu 355	Leu	Met	Arg	Ser	Asn 360	Ala	Ala	Leu	Phe	Gln 365	Leu	Gly	Ser
Ala	Pro 370	Ala	Val	Cys	Trp	Ile 375	Val	Cys	Thr	Thr	Leu 380	Lys	Leu	Gln	Met
Glu 385	Lys	Gly	Glu	Asp	Pro 390	Val	Pro	Thr	Cys	Leu 395	Thr	Arg	Thr	Gly	Leu 400
Phe	Leu	Arg	Phe	Leu 405	Cys	Ser	Arg	Phe	Pro 410	Gln	Gly	Ala	Gln	Leu 415	Arg
Gly	Ala	Leu	Arg 420	Thr	Leu	Ser	Leu	Leu 425	Ala	Ala	Gln	Gly	Leu 430	Trp	Ala
		435					440	_				445	-	Val	
	450					455		_	_	_	460		_	Gln	-
465					470					475				Gln	480
				485		_			490	_				Glu 495	•
			500					505					510	Leu	
		515					520					525		Tyr	
	530					535					540			Ala	
545					550		_		_	555				Arg	560
				565					570					Gln 575	
			580					585					590	Lys	
		595					600					605		Val	
	610					615		_		•	620			Gln	-
625					630					635				Thr	640
				645					650					His 655	
			660					665			-		670	Lys	_
		675					680					685		Leu	
	690					695					700			Gln	
val	val	rhe	ьys	Asn	lie	Ser	Pro	Ala	Asp	Ala	His	Arg	Asn	Leu	Cys

705	7.1 -	т о	7	C1	710	T	m)	17 - 1	(T) }-	715	7	æ,	Ţ	G 1	720	
reu	Ald	reu	Arg	725	His	гуѕ	IIII	vai	730	ryr	Leu	Inr	Leu	735	GIÀ	
Asn	Asp	Gln	Asp 740		Met	Phe	Pro	Ala 745		Cys	Glu	Val	Leu 750		His	
Pro	Glu	Cys 755	Asn	Leu	Arg	Tyr	Leu 760	Gly	Leu	Val	Ser	Cys 765		Ala	Thr	
Thr	Gln 770	Gln	Trp	Ala	Asp	Leu 775	Ser	Leu	Ala	Leu	Glu 780	Val	Asn	Gln	Ser	
Leu 785	Thr	Cys	Val	Asn	Leu 790	Ser	Asp	Asn	Glu	Leu 795	Leu	Asp	Glu	Gly	Ala 800	
				805	Thr				810					815		
			820		Cys			825					830			
		835			Val		840					845	_			
	850				Asn	855	•		_		860	-		_		
865					Lys 870					875				•	880	
				885	Cys				890					895	_	
			900		Leu			905					910			
		915			Cys		920					925				
	930				Trp	935					940			-		
945	Leu	Cys	261	NIA	950	261	Mall	GIII	Sel	955	vaı	1111	reu	Asp	960	
Gly	Gln	Asn	Pro	Leu 965	Gly	Ser	Ser	Gly	Val 970	Lys	Met	Leu	Phe	Glu 975		
			980		Gly			985			_		990		-	
		995			Leu		1000)				1005	5			
	1010)			Ile	1015	5		Lys	His	His 1020		Trp	Ala	Glu	
Arg 1025		Ser	Ser	HIS	Asp 1030		Met	He								
<213 <212	0> 3 1> 30 2> DN 3> Ho	1A	sapie	ens												
<400 atg		ca a	accto	icado	ac to	etaat	.ggad	r cac	actica	acc	agga	atdad	att d	ragca	agttc	60
															aggag	120
															agctac	180
															ctgag cctcta	240 300
															gagege	360
ttca	aaaa	cag a	agca	acaaq	ga da	aaga	caat	agg	gtgca	iggt	atat	atto	gaa 🤄	gacga	agttc	420
															gagaga :acacg	480 540
	gu	.90	guit	Jocai		.gcac		- 495	ام د کار		ccgc	gucc		Juai	ucacy	240

```
600
gtggtgctgt atggtdctgc aggcettggg aaaaccaege tggeecagaa actaatgeta
gactgggcag aggacaacct catccacaaa ttcaaatatg cgttctacct cagctgcagg
                                                                       660
gageteagee geetgggeee gtgeagtttt geagagetgg tetteaggga etggeetgaa
                                                                       720
ttgcaggatg acattecaca cateetagee caageaegga aaatettgtt egtgattgae
                                                                       780
ggctttgatg agctgggagc cgcacctggg gcgctgatcg aggacatctg cggggactgg
                                                                       840
gagaagaaga agcoggtgoo ogtootootg gggagtttgo tgaacagggt gatgttacoo
                                                                       900
aaggeegeee tgetggteae eaegeggeee agggeeetga gggaeeteeg gateetggeg
                                                                       960
gaggageega tetacataag ggtggaggge tteetggagg aggacaagag ggeetattte
                                                                      1020
ctgagacact ttggagacga ggaccaagcc atgcgtgcct ttgagctaat gaggagcaac
                                                                      1080
gaggeeetgt tecagetggg eteggeeece gaggtgtget ggatagtgtg caagaatatg
                                                                      1140
aagctgcaga tggagaaggg ggaggacccg gtccccacct gcctcacccg cacggggctg
                                                                      1200
tteetgegtt teetetgeag eeggtteeeg eagggegeae agetgeggg egegetgegg
                                                                      1260
acgetgagee teetggeege geagggeetg tgggegeaga egteegtget teacegagag
                                                                      1320
gatetggaaa ggeteggggt geaggagtee gaceteegte tgtteetgga eggagaeate
                                                                      1380
ctccgccagg acagagtete caaaggetge tactcettea tecaceteag ettecageag
                                                                      1440
tttctcactg ccctgttcta caccctggag aaggaggagg aagaggatag ggacggccac
                                                                      1500
                                                                      1560
acctgggaca ttggggacgt acagaagctg ctttccggag tagaaagact caggaacccc
gacctgatee aagcaggeta etacteettt ggeetegeta acgagaagag agccaaggag
                                                                      1620
ttggaggcca cttttggctg ccggatgtca ccggacatca aacaggaatt gctgcgatgc
                                                                      1680
gacataagtt gtaagggtgg acattcaacg gtgacagacc tgcaggagct cctcggctgt
                                                                      1740
ctgtacgagt ctcaggagga ggagctggtg aaggaggtga tggctcagtt caaagaaata
                                                                      1800
tecetgeact taaatgeagt agaegttgtg ceatetteat tetgegteaa geactgtega
                                                                      1860
aacctgcaga aaatgtcact gcaggtaata aaggagaatc tcccggagaa tgtcactgcg
                                                                      1920
tetgaateag aegeegaggt tgagagatee eaggatgate ageaeatget teetttetgg
                                                                      1980
acggaccttt gttccatatt tggatcaaat aaggatctga tgggtctagc aatcaatgat
                                                                      2040
agetttetea gtgeeteeet agtaaggate etgtgtgaae aaatageete tgacaeetgt
                                                                      2100
catctccaga gagtggtgtt caaaaacatt tccccagetg atgctcateg gaacctctgc
                                                                      2160
ctagetette gaggteacaa gaetgtaaeg tatetgaeee tteaaggeaa tgaeeaggat
                                                                      2220
gatatgtttc ccgcattgtg tgaggtcttg agacatccag aatgtaacct gcgatatctc
                                                                      2280
gggttggtgt cttgttccgc taccactcag cagtgggctg atctctcctt ggcccttgaa
                                                                      2340
gtcaaccagt cectgaegtg egtaaacete teegacaatg agettetgga tgagggtget
                                                                      2400
                                                                      2460
aagttgetgt acacaacttt gagacacece aagtgettte tgeagaggtt gtegttggaa
aactgtcacc ttacagaagc caattgcaag gaccttgctg ctgttgttggt tgtcagccgg
                                                                      2520
gagetgacae acetgtgett ggeeaagaae eecattggga atacaggggt gaagtttetg
                                                                      2580
tgtgaggget tgaggtacce egagtgtaaa etgeagacet tggtgetttg gaaetgegae
                                                                      2640
ataactageg atggetgetg egateteaca aagettetee aagaaaaate aageetgttg
                                                                      2700
tgtttggatc tggggctgaa tcacatagga gttaagggaa tgaagtteet gtgtgagget
                                                                      2760
ttgaggaaac cactgtgcaa cttgagatgt ctgtggttgt ggggatgttc catccctccg
                                                                      2820
ttcagttgtg aagacetetg etetgeeete ageaaceaga geetegteae tetggaeetg
                                                                      2880
ggtcagaatc cettggggte tagtggagtg aagatgetgt ttgaaacett gacatgttee
                                                                      2940
                                                                      3000
agtggcaccc tccggacact caggttgaaa atcgatgact ttaatgatga actcaataag
                                                                      3060
ctgctggaag aaatagaaga aaaaaaccca caactgatta ttgatactga gaaacatcat
                                                                      3099
ccctgggcag aaaggccttc ttctcatgac ttcatgatc
<210> 4
<211> 3857
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (139)...(3240)
<400> 4
ccacgegtee geocacgegt cogggeatet ggggaaacet ttettecatg geteaggaea
                                                                       60
cacteetgga tegageeaac aggagaaett tetgtgtgga eegaageeta aggaeeetga
                                                                      120
aaacagetge agatgaag atg gea age ace ege tge aag etg gee agg tae
                                                                      171
```

		Met 1	Ala	Ser	Thr	Arg 5	Cys	Lys	Leu	Ala	Arg 10	Tyr	
		gat Asp											219
		cag Gln											267
		cat His											315
		gcg Ala 65											363
		ctt Leu											411
		gca Ala											459
		gag Glu											507
		aaa Lys											555
		aga Arg 145											603
		agc Ser											651
		agc Ser											699
		acg Thr											747
		ccc Pro											795
		gcg Ala											843

220				225				230			235	
										agg Arg 250		891
										aca Thr		939
										aac Asn		987
					_			_		ctc Leu	-	1035
										gga Gly		1083
										ctg Leu 330		1131
										atc Ile		1179
										cat His		1227
								_		gag Glu		1275
										ttc Phe		1323
										ccc Pro 410		1371
										agt Ser		1419
	-	_	_			-			 	gtc Val		1467
										cac His		1515

							gga Gly		1563
							cat His 490		1611
							ttc Phe		1659
							act Thr		1707
							aag Lys		1755
							cga Arg		1803
							tat Tyr 570		1851
							agg Arg		1899
							atc Ile		1947
							aag Lys	-	1995
							gag Glu		2043
							aag Lys 650		2091
							ttt Phe		2139
							ctc Leu		2187

	atg Met 685															2235
	atg Met		_	_	-			_				-	-	-		2283
	gga Gly															2331
	tca Ser															2379
	aat Asn															2427
	cat His 765			_				-	-		_		_	-	3 3	2475
	tcg Ser															2523
	aag Lys															2571
	atc Ile										-	-	-		-	2619
	aag Lys															2667
	ctt Leu 845															2715
	ggg Gly															2763
	gcc Ala															2811
	ggc Gly															2859
act	aat	cag	aat	ctc	acg	cac	ctt	tac	ctg	cga	ggc	aac	act	ctc	gga	2907

Thr Asn Gln Asn Leu Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly 910 915 920												
gac aag ggg atc aaa cta ctc tgt gag gga ctc ttg cac ccc gac tgc Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys 925 930 935	2955											
aag ott oag gtg ttg gaa tta gao aac tgo aac oto acg toa oac tgo Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys 940 955	3003											
tgc tgg gat ctt tcc aca ctt ctg acc tcc agc cag agc ctg cga aag Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg Lys 960 965 970	3051											
ctg agc ctg ggc aac aat gac ctg ggc gac ctg ggg gtc atg atg ttc Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe 975 980 985	3099											
tgt gaa gtg ctg aaa cag cag agc tgc ctc ctg cag aac ctg ggg ttg Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu 990 995 1000	3147											
tct gaa atg tat ttc aat tat gag aca aaa agt gcg tta gaa aca ctt Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu 1005 1010 1015	3195											
caa gaa gaa aag cct gag ctg acc gtc gtc ttt gag cct tct tgg Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro Ser Trp 1020 1025 1030	3240											
taggagtgga aacggggctg ccagacgcca gtgttctccg gtccctccag ctgggggccc tcaggtggag agagctgcga tccatccagg ccaagaccac agctctgtga tccttccggt ggagtgtcgg agaagagag ttgccgacga tgccttcctg tgcagagctt gggcatctcc tttacgccag ggtgaggaag acaccaggac aatgacagca tcgggtgttg ttctcatcac agcgcctcag ttagaggatg ttcctcttgg tgacctcatg taattagctc attcaataaa gcactttctt tattttctc ttctctgtct aactttctt ttcctatctt tttttctct ttgttctgtt tacttttgct catacatca ttcccgctaa ctttctatta actgaccata acacagaact agttgactat atattatgtt gaaattttat ggcagctatt tatttatta aatttttgt aatagtttg ttttctaata agaaaaatcc atggttttg tagctggttg ttaaaaaaaaa actttttggt atttaattaa attgattcct ttcttaatt ttaaaaaaaaa actttttggt atttaattaa attgattcct tttcttaatt ttaaaaaaaaa	3300 3360 3420 3480 3540 3600 3660 3720 3780 3840 3857											
<210> 5 <211> 1034 <212> PRT <213> Homo sapiens												
<400> 5												
Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr Leu Glu Asp Leu Glu 1 10 15												
Asp Val Asp Leu Lys Lys Phe Lys Met His Leu Glu Asp Tyr Pro Pro 20 25 30												
Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln Thr Glu Lys Ala Asp 35 40 45												
His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys 50 55 60												

						_		_	_		_				
Ala 65	Trp	Ala	Met	Ala	Val 70	Trp	Ile	Phe	Ala	Ala 75	Ile	Asn	Arg	Arg	Asp 80
Leu	Tyr	Glu	Lys	Ala 85	Lys	Arg	Asp	Glu	Pro 90	Lys	Trp	Gly	Ser	Asp 95	Asn
Ala	Arg	Val	Ser 100	Asn	Pro	Thr	Val	Ile 105	Cys	Gln	Glu	Asp	Ser 110	Ile	Glu
Glu	Glu	Trp 115	Met	Gly	Leu	Leu	Glu 120	Tyr	Leu	Ser	Arg	Ile 125	Ser	Ile	Cys
Lys	Met 130	Lys	Lys	Asp	Tyr	Arg 135	Lys	Lys	Tyr	Arg	Lys 140	Tyr	Val	Arg	Ser
Arg 145	Phe	Gln	Cys	Ile	Glu 150	Asp	Arg	Asn	Ala	Arg 155	Leu	Gly	Glu	Ser	Val 160
Ser	Leu	Asn	Lys	Arg 165	Tyr	Thr	Arg	Leu	Arg 170	Leu	Ile	Lys	Glu	His 175	Arg
Ser	Gln	Gln	Glu 180	Arg	Glu	Gln	Glu	Leu 185	Leu	Ala	Ile	Gly	Lys 190	Thr	Lys
Thr	Cys	Glu 195	Ser	Pro	Val	Ser	Pro 200	Ile	Lys	Met	Glu	Leu 205	Leu	Phe	Asp
Pro	Asp 210	Asp	Glu	His	Ser	Glu 215	Pro	Val	His	Thr	Val 220	Val	Phe	Gln	Gly
Ala 225	Ala	Gly	Ile	Gly	Lys 230	Thr	Ile	Leu	Ala	Arg 235	Lys	Met	Met	Leu	Asp 240
Trp	Ala	Ser	Gly	Thr 245	Leu	Tyr	Gln	Asp	Arg 250	Phe	Asp	Tyr	Leu	Phe 255	Tyr
Ile	His	Cys	Arg 260	Glu	Val	Ser	Leu	Val 265	Thr	Gln	Arg	Ser	Leu 270	Gly	Asp
Leu	Ile	Met 275	Ser	Cys	Суѕ	Pro	Asp 280	Pro	Asn	Pro	Pro	Ile 285	His	Lys	Ile
	290				_	Ile 295					300	_		-	
305					310	Glu				315					320
Gln	Lys	Ala	Glu	Arg 325	Gly	Asp	Ile	Leu	Leu 330	Ser	Ser	Leu	Ile	Arg 335	Lys
Lys	Leu	Leu	Pro 340	Glu	Ala	Ser	Leu	Leu 345	Ile	Thr	Thr	Arg	Pro 350	Val	Ala
		355				Leu	360	_			_	365			
	370					Lys 375					380			_	
385					390	Arg				395					400
Glu	Val	Leu	Phe	Thr 405	Met	Cys	Phe	Ile	Pro 410	Leu	Val	Cys	Trp	Ile 415	Val
			420			Gln		425		_	_		430		
		435				Ala	440	-				445			
	450		-	_	_	Ser 455				_	460	_			
465	_		_		470	Ala		-	_	475	_			_	480
				485		Leu			490	_			_	495	_
			500			Met		505			_		510	_	_
Glu	Lys	Phe	Tyr	Ser	Phe	Ile	His	Met	Thr	Phe	Gln	Glu	Phe	Phe	Ala

		515					520					525			
Ala	Met 530	Tyr	Tyr	Leu	Leu	Glu 535	Glu	Glu	Lys	Glu	Gly 540	Arg	Thr	Asn	Val
Pro 545	Gly	Ser	Arg	Leu	Lys 550	Leu	Pro	Ser	Arg	Asp 555	Val	Thr	Val	Leu	Leu 560
Glu	Asn	Tyr	Gly	Lys 565	Phe	Glu	Lys	Gly	Tyr 570	Leu	Ile	Phe	Val	Val 575	Arg
			Gly 580					585					590		
Lys	Leu	Ser 595	Cys	Lys	Ile	Ser	Gln 600	Gln	Ile	Arg	Leu	Glu 605	Leu	Leu	Lys
Trp	Ile 610	Glu	Val	Lys	Ala	Lys 615	Ala	Lys	Lys	Leu	Gln 620	Ile	Gln	Pro	Ser
625			Leu		630					635				_	640
			Ala	645					650					655	
			Asp 660					665					670	_	
		675	Ser				680					685		_	
	690		Glu			695					700				
705			Ser		710				-	715		-			720
			Thr	725			-	-	730					735	
			Ser 740					745					750		_
		755	Met	_			760					765		_	-
	770		Arg			775			_	_	780				-
785			Ile Ser		790					795		_			800
	_		Leu	805				_	810		-		-	815	
			820 Cys					825					830		
		835	Ser				840					845			
	850		Ser			855		_		_	860	_			
865			Leu		870				_	875	_		•		880
			Ser	885					890					895	
			900 Tyr					905					910		
		915	Glu				920					925	_		-
	930		Asn			935					940				
945			Thr		950					955					960
				965					970	-,5	204			975	

```
Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe Cys Glu Val Leu Lys
            980
                                985
                                                    990
Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu Ser Glu Met Tyr Phe
                            1000
                                                1005
Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu Gln Glu Glu Lys Pro
    1010
                        1015
                                            1020
Glu Leu Thr Val Val Phe Glu Pro Ser Trp
1025
                    1030
<210> 6
<211> 3102
<212> DNA
<213> Homo sapiens
<400> 6
atggcaagca cccgctgcaa gctggccagg tacctggagg acctggagga tgtggacttg
                                                                        60
aagaaattta agatgcactt agaggactat cotcoccaga agggctgcat coccctcccg
                                                                       120
                                                                       180
aggggtcaga cagagaaggc agaccatgtg gatctagcca cgctaatgat cgacttcaat
ggggaggaga aggcgtgggc catggccgtg tggatcttcg ctgcgatcaa caggagagac
                                                                       240
ctttatgaga aagcaaaaag agatgagccg aagtggggtt cagataatgc acgtgtttcg
                                                                       300
aatcccactg tgatatgcca ggaagacagc attgaagagg agtggatggg tttactggag
                                                                       360
tacctttcga gaatctctat ttgtaaaatg aagaaagatt accgtaagaa gtacagaaag
                                                                       420
tacgtgagaa gcagattcca gtgcattgaa gacaggaatg cccgtctggg tgagagtgtg
                                                                       480
agecteaaca aacgctacac acgactgegt eteateaagg ageaceggag eeageaggag
                                                                       540
agggagcagg agettetgge categgeaag accaagaegt gtgagageee egtgagteee
                                                                       600
attaagatgg agttgctgtt tgaccccgat gatgagcatt ctgagcctgt gcacaccgtg
                                                                       660
gtgttccagg gggcggcagg gattgggaaa acaatcctgg ccaggaagat gatgttggac
                                                                       720
tgggcatcgg ggacactcta ccaagacagg tttgactatc tgttctatat ccactgtcgg
                                                                       780
gaggtgagcc ttgtgacaca gaggagcctg ggggacctga tcatgagctg ctgccccgac
                                                                       840
ccaaacccac ccatccacaa gatcgtgaga aaaccctcca gaatcctctt cctcatggac
                                                                       900
ggettegatg agetgeaagg tgeetttgae gageacatag gaeegetetg caetgaetgg
                                                                       960
cagaaggccg agcggggaga catteteetg agcageetea teagaaagaa getgetteee
                                                                      1020
gaggeetete tgeteateae caegagaeet gtggeeetgg agaaaetgea geaettgetg
                                                                      1080
gaccatcctc ggcatgtgga gatcctgggt ttctccgagg ccaaaaggaa agagtacttc
                                                                      1140
                                                                      1200
ttcaagtact tctctgatga ggcccaagcc agggcagcct tcagtctgat tcaggagaac
gaggteetet teaceatgtg etteateece etggtetget ggategtgtg caetggaetg
                                                                      1260
aaacagcaga tggagagtgg caagagcctt gcccagacat ctaagaccac caccgcggtg
                                                                      1320
tacgtettet teettteeag tttgetgeag eeceggggag ggageeagga geaeggeete
                                                                      1380
tgcgcccacc tctgggggct ctgctctttg gctgcagatg gaatctggaa ccagaaaatc
                                                                      1440
ctgtttgagg agtccgacct caggaatcat ggactgcaga aggcggatgt gtctgctttc
                                                                      1500
                                                                      1560
ctgaggatga acctgttcca aaaggaagtg gactgcgaga agttctacag cttcatccac
atgactitice aggagitett tgeegeeatg tactacetge tggaagagga aaaggaagga
                                                                      1620
                                                                      1680
aygacgaacg ttccagggag tcgtttgaag cttcccagcc gagacgtgac agtccttctg
gaaaactatg gcaaattcga aaaggggtat ttgatttttg ttgtacgttt cctctttggc
                                                                      1740
ctggtaaacc aggagaggac ctcctacttg gagaagaaat taagttgcaa gatctctcag
                                                                      1800
caaatcaggc tggagctgct gaaatggatt gaagtgaaag ccaaagctaa aaagctgcag
                                                                      1860
atccagccca gccagctgga attgttctac tgtttgtacg agatgcagga ggaggacttc
                                                                      1920
gtgcaaaggg ccatggacta tttccccaag attgagatca atctctccac cagaatggac
                                                                      1980
cacatggttt cttccttttg cattgagaac tgtcatcggg tggagtcact gtccctgggg
                                                                      2040
                                                                      2100
tttctccata acatgcccaa ggaggaagag gaggaggaaa aggaaggccg acaccttgat
atggtgcagt gtgtcctccc aagctcctct catgctgcct gttctcatgg attggtgaac
                                                                      2160
                                                                      2220
agccacctca cttccagttt ttgccggggc ctcttttcag ttctgagcac cagccagagt
ctaactgaat tggacctcag tgacaattct ctgggggacc cagggatgag agtgttgtgt
                                                                      2280
                                                                      2340
gaaacgctcc agcatcctgg ctgtaacatt cggagattgt ggttggggcg ctgtggcctc
togoatgagt gotgottoga catotoottg gtootcagca goaaccagaa gotggtggag
                                                                      2400
ctggacctga gtgacaacgc cetcggtgac ttcggaatca gacttctgtg tgtgggactg
                                                                      2460
aagcacctgt tgtgcaatct gaagaagctc tggttggtca gctgctgcct cacatcagca
                                                                      2520
```

2580

2700

2760

2820

2880

2940

3000

3060

```
tgttgtcagg atettgcatc agtattgagc accagccatt ccctgaccag actctatgtg
ggggagaatg cettgggaga etcaggagte geaattttat gtgaaaaage caagaateea
cagtgtaacc tgcagaaact ggggttggtg aattctggcc ttacgtcagt ctgttgttca
getttgteet eggtaeteag cactaateag aateteaege acetttaeet gegaggeaae
actoteggag acaaggggat caaactacto tgtgagggac tottgcacco egactgcaag
cttcaggtgt tggaattaga caactgcaac ctcacgtcac actgctgctg ggatctttcc
acacttetga ectecageca gageetgega aagetgagee tgggeaacaa tgaeetggge
gacctggggg teatgatgtt etgtgaagtg etgaaacage agagetgeet eetgeagaae
ctggggttgt ctgaaatgta tttcaattat gagacaaaaa gtgcgttaga aacacttcaa
gaagaaaagc ctgagctgac cgtcgtcttt gagccttctt gg
<210> 7
<211> 77
<212> PRT
<213> Homo sapiens
<400> 7
Asp His Leu Ser Thr Leu Glu Glu Leu Val Pro Tyr Asp Phe Glu
Lys Phe Lys Phe Lys Leu Gln Asn Thr Ser Val Gln Lys Glu His Ser
                                25
Arg Ile Pro Arg Ser Gln Ile Gln Arg Ala Arg Pro Val Lys Met Ala
Thr Leu Leu Val Thr Tyr Tyr Gly Glu Glu Tyr Ala Val Gln Leu Thr
                        55
Leu Gln Val Leu Arg Ala Ile Asn Gln Arg Leu Leu Ala
                    7.0
<210> 8
<211> 77
<212> PRT
<213> Homo sapiens
<400> 8
Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr Ala Glu Glu Leu Lys
                                    10
Lys Phe Lys Leu Lys Leu Ser Val Pro Leu Arg Glu Gly Tyr Gly
                                25
Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp Ala Leu Asp Leu Thr
Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr Gly Ala Glu Leu Thr
                        55
Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu Met Ala
                    70
<210> 9
<211> 77
<212> PRT
<213> Homo sapiens
<400> 9
Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu Leu Lys
                                    10
Glu Phe Gln Leu Leu Ala Asn Lys Ala His Ser Arg Ser Ser Ser
                                25
Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu Val Ala
                            40
```

```
Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln Arg Ala Trp Asp Leu Ala
                        55
Leu His Thr Trp Glu Gln Met Gly Leu Arg Ser Leu Cys
<210> 10
<211> 77
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any Amino Acid
<400> 10
Asp Xaa Leu Leu Xaa Xaa Leu Glu Xaa Leu Xaa Xaa Glu Glu Leu Lys
Lys Phe Lys Leu Leu Xaa Asn Xaa Ser Xaa Xaa Glu Xaa Ser
                                25
Arg Ile Pro Arg Xaa Gln Xaa Xaa Lys Ala Asp Gly Xaa Xaa Leu Ala
Xaa Xaa Leu Val Thr Xaa Tyr Gly Glu Xaa Tyr Ala Val Glu Leu Ala
                        55
Leu Gln Val Leu Glu Xaa Met Gly Leu Arg Xaa Leu Ala
                    70
<210> 11
<211> 77
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any Amino Acid
<400> 11
Asp Xaa Leu Ala Xaa Tyr Leu Glu Xaa Leu Xaa Xaa Glu Glu Leu Lys
                                   10
Lys Phe Lys Leu Leu Xaa Asn Xaa Ser Pro Gln Lys Gly Xaa Ser
                                25
Arg Ile Pro Arg Gly Gln Xaa Glu Lys Ala Asp Gly Val Asp Leu Ala
                            40
Thr Leu Leu Val Thr Phe Tyr Gly Glu Glu Tyr Ala Trp Ala Leu Ala
                        55
Leu Gln Val Leu Glu Ala Met Gly Leu Arg Asp Leu Ala
                    70
<210> 12
<211> 28
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Consensus sequence
<400> 12
Asn Pro Ser Leu Arg Glu Leu Asp Leu Ser Asn Asn Lys Leu Gly Asp
Glu Gly Ala Arg Ala Leu Ala Glu Ala Leu Lys Ser
            20
<210> 13
<211> 23
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<400> 13
Asn Leu Glu Glu Leu Asp Leu Ser Asn Asn Leu Thr Ser Leu Pro Pro
                                    10
Gly Leu Phe Ser Asn Leu Pro
            20
<210> 14
<211> 90
<212> PRT
<213> Homo sapiens
<400> 14
Met Ala Lys Thr Pro Ser Asp His Leu Leu Ser Thr Leu Glu Glu Leu
                                    10
Val Pro Tyr Asp Phe Glu Lys Phe Lys Phe Lys Leu Gln Asn Thr Ser
            20
                                25
Val Gln Lys Glu His Ser Arg Ile Pro Arg Ser Gln Ile Gln Arg Ala
                            40
Arg Pro Val Lys Met Ala Thr Leu Leu Val Thr Tyr Tyr Gly Glu Giu
                        55
Tyr Ala Val Gln Leu Thr Leu Gln Val Leu Arg Ala Ile Asn Gln Arg
                    70
Leu Leu Ala Glu Glu Leu His Arg Ala Ala
<210> 15
<211> 90
<212> PRT
<213> Homo sapiens
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
                                    10
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
                                25
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
                            40
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gin
```

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg 65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala 85 90

<210> 16

<211> 89

<212> PRT

<213> Homo sapiens

<400> 16

 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr

 1
 5
 10
 15

 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 20
 25
 30

 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 35
 40
 45

 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 50
 60

 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 65
 70
 75

Met Ala Gly Gln Leu Gln Ala Ala Thr 85

<210> 17

<211> 89

<212> PRT

<213> Homo sapiens

<400> 17

 Met
 Gly
 Thr
 Lys
 Arg
 Glu
 Ala
 Ile
 Leu
 Lys
 Val
 Leu
 Glu
 Asn
 Leu
 Thr

 Pro
 Glu
 Glu
 Leu
 Lys
 Lys
 Phe
 Lys
 Met
 Lys
 Leu
 Gly
 Thr
 Val
 Pro
 Leu

 Arg
 Glu
 Gly
 Phe
 Glu
 Arg
 Ile
 Pro
 Arg
 Gly
 Ala
 Leu
 Gly
 Glu
 Gly
 Glu
 Leu
 Asp
 Asp
 Tyr
 Glu
 Asp
 Tyr
 Glu
 Asp
 Met
 Leu
 Glu
 Ala
 Ala